

SEQUENCE LISTING

RECEIVED

MAR 1 5 2001

TECH CENTER 1600/2900

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<110> Parham, Christi L.
   Moore, Revin W.
   Murgolo, Nicholas J.
   Bazan, J. Fernando
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<120> Human Receptor Proteins; Related Reagents and Methods

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<140> 09/265,540
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<141> 1999-03-08

<160>, 6

<170> PatentIn Ver. 2.0

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<212> DNA

<213> primate

<220>

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<222> (132)..(1064)

<220>

<221> unsure

<222> (567)

<223> n at position 567; n may be A, C, G, or T; translated amino acid depends on genetic code

<220>

<221> unsure

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<223> n at position 573; n may be A, C, G, or T; translated amino acid depends on genetic code

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<223> n at position 1342; n may be A, C, G, or T; translated amino acid depends on genetic code

B

Bynt

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atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile agc tgc aga agg gag gtg gat gcc tgt gcc acg gct gtg atg tct

By

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser 290 295 300

cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084
Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
305

ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gaggggacaa gttgtgttt 1144

tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgtc tacaagtcta 1204

gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264

gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324

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Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val 20 25 30

Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met 35 40 45

Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val 50

Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser 65 70 75 80

His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
85 90 95

Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg 100 105 110

Bh

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<211> 311

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<213> primate

Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser

By.

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<222> (2)..(694)

<220>

<221> unsure

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Bt

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly

ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile 165 170 175 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp 180 185 190 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val 195 200 205 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr 210 215 220 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggct ctgagccgag 724 Gln Asn Ser Gly Ala Val Cys 225 230 gaagctgctg atgtccatgt cagcacttta tggaatccgg tcctccattt tcctgtcccc 784 aaaaggcccg tcagtgcctg tgaagatgta acgggtctca tgggggcgac aagcttattg 844 attttttttt tcaaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904 tatgtccccg aaagattaag atttctctta aacactaaaa agacatgtaa ttatttgtta 964 gcaaatgggc gtctggcacg cctctgacac tttttcgtca gcagccagga cacgaggtcc 1024 cctccttgat gaagcccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084 gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta 1144 aatagtttca cagagattaa gccttttttt cccccaagtt aggaataaaa gactataatt 1204 aactttttaa aaaaaaaaa aaaaaaaaa aaaaa'aaaaa 1244

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<211> 231

<212> PRT

<213> primate

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Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro 35

Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa 50 55

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn 65 70 75 80

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln 85 90 95

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly 100 105

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr 115 120 125

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu 130 135 140

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly 145 150 150

Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile 165 170 175

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp 180 185 190

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val . 195 200 205

Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr 210 220

Gln Asn Ser Gly Ala Val Cys 225 230

But

<210> 5

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<213> primate

<400> 5

Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Leu Gly Val Phe 1 5 15

Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala 20 25 30

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser 35

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg 50

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met 65 70 75 80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
85 90 95

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr 100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr 115 120 125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu 130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser 145 150 155

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr 165

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe 180 185 190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr 195 200 205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe 210 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp 230 235 240

But

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe 245 250 255

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys 260 265 270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro 275 280 285

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu 290 295 300

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Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr 325 330 335

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<211> 325

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Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly 35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp 50

Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser 65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu 85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile 100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His 115 120 125

Byt

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr Ash Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr Asp Glu Lys\Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly Cys Phe Ser Leu Leu Trp Cys Vall Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser Gly Lys Gln Asn Pro Gly Asp Ser Cy\$ Ser Leu Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser

FILE COPY

BIOTECHNO GO SYSTEMS BRANCH 01-11-c

RAW SEQUENCE LISTING

ERROR REPORT

MAR 0 7 2001

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JAN 10 2001

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/

09/265,5400

Source:

Date Processed by STIC:

1643

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail belp: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

FFR 22 '01 03:49

TOT TOD DOT

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SERIAL NUMBER: 09/265,540C

Raw Sequence Listing Error Jummary

ERROR DETECTED SUGGESTED CORRECTION

ATTA	I: NEW RULES CASES: I	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED B	Y PTO SOFTWARE
1	Wrapped Nuclcles	The number/lext at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	RECEIVED
2	_ Wrapped Aminos	The amino acid number/lext at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it.	JAN 10 mng
	•	Please adjust your right margin to .3, as this will prevent "wrapping".	TECH CENTS
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces	. .
4	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the between the numbering. It is recommended to delete any labs and use spacing between	
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be pre-	ocessed.
6	Variable Length -	Sequence(s) contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7	Palenlin ver. 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from sequence(s) Normally, Patentin would automatically generate this sequencely coded nucleic acid sequence. Please manually copy the relevant <220>-<10 the subsequent amino acid sequence. This applies primarily to the mandatory sections for Artificial or Unknown sequences.	ction from the_ 223> section
8	Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please use the following format for each skip (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENC (xl) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped	,
	•.	Please also adjust the "(III) NUMBER OF SEQUENCES:" response to include the skip	ped sequence(s).
9	Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please use the following format for each skip <210> sequence id number <400> sequence id number 000	ped sequence.
10	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or	r Xaa represents.
11	Use of <213>Organism (NEW RULES)	Sequence(s) are missing this mandatory field or its response.	
12	Use of <220>Feature (NEW RULES)	Sequence(s) are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGAŅISM is "Artificial" or "Unknown Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)	(Sec. 1.823 of new Rules)
13	Palentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a file; Testing in missing mandatory numeric identifiers and responses (as indicated on Instead, please use "File Manager" or any other means to copy file to floppy disk.	•

AKS-Biotechnology Systems Branch-5/15/99

FFR 22 '01 03:49

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Page 1 of 7





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1643

JAN 1 0 2001

BAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540C

DATE: 01/04/2001 MIMF: 12:53:41

TECH CENTER 1600/2900

luput Sat : A:\804k.app

Output Set: N:/CRF3/01022001/1364540C. raw

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I SITO, APPLICANT: Parham, Christi L.
          Hoore, Kevin W
          Hurgalo, Michalas J.
          Tarlan I. Egrando
 B 2170% PIPER OF INVENTION: Human Receptor Processes Related Reagents and Matheda
10 -130> FILE REFERENCE: DX0801K
12 GLIOF CURPRIES FOR ACAPTON NUMBER: 09/265,546C
TO THE CHERENT FOUND DAME: 1999-03-08
15 - Tour number of 840 in 408 6
17 SL70> SOMEWARE'S Paleolith Voc. 2.0
19 ×210× 360 10 No: 1
20 × 2112 TEHRTH: 1361
コナー・ストラッ リメトビューレバン
32 <214> ORCANISM: primate
24 (220) PERFORE:
25 2215 NAMEYKEYE COS
26 #022> LOCATION: (132)..(1061)
28 +220> PEATORE:
29 CARLO BARRIZKEY: Girc_Foatura
30 · 222× LOCATION: (557)
3% 22.3\% OTHER INFORMATION to all position 567) is may be \Lambda_{\rm b} C. G. of \Psi_{
m c}
          translated amino acid depends on genetic code
11:
ナト ふことりさ トじんりりんしょ
35 -337 - MARRIKAT: misc. fcature
76 KILIA DOCATION: (473)
17 CP21% OPER INFORMATION: IT all position 573; It may be A. C. G. or T.
         transtaund amino weld depends on genetic code
13
    320× PRATUREL
11 .3x1> NAME/KRY: mistc_loature
42 (222) LOCATION: (1336)
43 (23%) OTHER INFORMATION: it all position 14% to may be A.d. G. of T.
         translated amino acid depends on genetic code
46 C220% PRAMURE:
17 (23) - NADIZENY: migr_leature
48 <222% LOCATION: (1412)
19 -313 OTHER INCORNATIONS a at position 1342; a may be A. C. G. or T.
         translated amino acid depends on genetic code
93 Garde Frature:
50 <2215 NAME/KEY, misc<sub>el</sub>feathers
54 *223* LOCATION: (1469)
55 JO232 OTHER ENEORITATIONS of all possiblion faffer manage by A. C. C. of the
         translated unino acid depends on genetic code
50
58 FADUS SPORRICH: 1
55 (cquecence) og begeget gestettengn vellomprice uncaratyer tileligaugsa (b.
61 agalgreiga galggasaga Algelliatt 'tiggavagaa acaatgriet oqqibaadet 100
63 gaqteracea n atq enq ant lle aca ntq qit eta qua qua ate iqq pen 170
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Does Not Comply Corrected Diskette Needed

1/2/01

Page 2 of 7





RAW SEQUENCE LISTING PATENT 01/02/2001 PATENT APPLICATION: US/09/265,540C PIFFE: 12:23:11

Input Set : A:\804k.app

Output Sol: N:\CRE2\01022001\1265540C.raw

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Input Set : Ar\804k.app

Output Set: N:\CRF3\01022001\1265540C.Idw

L: 99 H: 34L W: (48) "n" or "Kaa" meed, for SP9 that 1:100 pa (4) we (40) "n" or "Saa" used, for any time: t 1.: 104 m: 341 W (40) " ' or "Kap" used, for spa inv. (1:116 H: 111 W: (16) " or "Nau" used, for applying ? L:120 (1:341 W: (10) "h" or "Sau" mich. for 880 (0):1 1.: [5] H: 14] W: (46) """ Or "Ada" usod, for she the:] L:15/ M:25% W: Mandatory Feature missing, 1250% not found for 180 104:3 E. THE HIPSH W. Handatory Feature missing, (22); not found for Sig Ipple Loans Roads W: Mandatory Fearone missing, 22222 not loans for SEO LDE:3 1:187 M 258 W. Mandatory Posture missing, <223, not found for stor tobjit 1.. 197 H: 340 W: (16) "h" OF "Maa" used: feature required, for \$100 ftm.2 10:100 M 258 W: Mandator Sualure missing, 22208 not found for sup that2 Little M:258 W: Mandatory Feature missing, .221, not Lound for SPO LDE.3 1::190 H:258 W: Mandatory Posture missing, 2000; not remod for SEQ Three 1.190 M:250 W. Mandatory tenture massing, 2233 not found for SEC 110.2 M: 340 Repeated in Seque-2 1::199 H: 258 W: Handstory Francic missing, .. 220% not found for SEO 108:2 T:199 H:258 W: Gandatory Posture missing, w2215 not found for SEC TDE:2 L:199 M:258 W: handator, Sective missing, -2225 not tound for Sec ibid 1:199 M:298 W: Randatory Feature missing, -2235 not found for SEQ 108:2 1.202 M. 198 W. Mandatory Frature missing, - 220, not found for Star (Driz 1,: 202 0: 258 W: Mandalory Vealure missing, 32212 not tound for Sec 110.12 figure M: 258 N: Mandatory Feature missing, 10 135 not round for SEQ The: 2 1. 203 M-258 We handstory bosture missing, 52235 not found for 980 ths:2 hards Harastory Fourier missing, 18232 not found for sho that? hills Wisto W (46) Wha of "Xeen mond: teature required, for SEO 104:3 to 195 M: 254 W: Mandalory Contact missing, (220) not found for 919 tok: 4 h: 12% H: 25m W: Kandarory Feature missing, 3001; not found for SEQ TEN: 4 4-335 H:258 W: Mandatory Posture ministing, -222% not found for SEO 104:1 1:325 H:258 M: Mandatory Feature missing, 2233, not found for Sky inp:4 u. 125 M. 140 W: (46) "h" or "Xaa" much: Posture required, for SEO IDE:1

